Please amend the application as follows and to comply with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures in adherence with rules 37 C.F.R. § 1.821-1.825:

IN THE SPECIFICATION:

Please delete the first submitted Sequence Listing in its entirety and replace it with the enclosed text, entitled "SEQUENCE LISTING."

REMARKS

The specification has been amended to correct errors in the Sequence Listing as reported in the Raw Sequence Listing Error Summary. Entry of this amendment is respectfully requested. This amendment is made in adherence with 37 C.F.R. § 1.821-1.825. This amendment is accompanied by a floppy disk containing the above named revised "Sequence Listing," SEQUENCE ID NUMBERS 1-85, in computer readable form, and a paper copy of the revised "Sequence Listing." The computer readable sequence listing was prepared through use of the software program "PatentIn" provided by the PTO. The information contained in the computer readable disk is identical to that of the paper copy as revised. The revised "Sequence Listing" is provided to comply with the sequence rules and contains no new matter. Applicant submits that this amendment, the accompanying computer readable sequence listing, and the paper copy thereof serve to place this application in a condition of adherence to the rules 37 C.F.R. § 1.821-1.825.

Please direct any calls in connection with this application to the undersigned at (415) 781-1989.

Respectfully submitted,

FLEHR HOHBACH TEST
ALBRITTON & HERBERT LLP

Dated: 3/20/02

Robin M. Silva
Reg. No. 38,304

Four Embarcadero Center
Suite 3400
San Francisco, CA 94111-4187
Telephone: (415) 781-1989

1078042

MAR 2 6 2002
PATENT & TRADEMARK OFFICE

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/710,058	11/10/2000	David Anderson	A-68531-1/RMS/JJD/SPL	4112

7590 02/27/2002

Flehr Hohbach Test Albritton & Herbert LLP
Suite 3400
Four Embarcadero Center
San Francisco, CA 94111-4187

EXAMINER
CELSA, BENNETT M

ART UNIT	PAPER NUMBER
1627	

DATE MAILED: 02/27/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/710,058			

OIPE JC54
MAR 26 2002
PATENT & TRADEMARK OFFICE

EXAMINER	
ART UNIT	PAPER NUMBER
1627	5

Please find below a communication from the EXAMINER in charge of this application

Sequence Rule Compliance: Bonafide Attempt Letter

Applicant's computer readable form (CRF) has been received. However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures and **RAW SEQUENCE LISTING ERROR REPORT.**

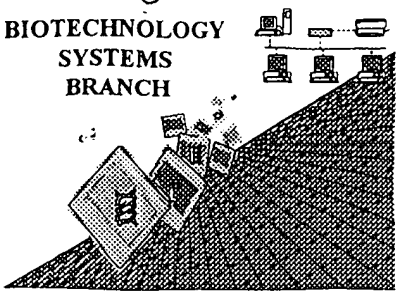
APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556 If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Venkat whose telephone number is (703) 308-0570. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Bennett Celsa (au 1627) (Feb. 25,2002)

BENNETT CELSA
PRIMARY EXAMINER

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

O I PE
MAR 2 6 2002
TC3400
PATENT & TRADEMARK OFFICE

#4

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/710,058

Source: 1646

Date Processed by STIC: 4/24/2001

RECEIVED
MAY 0 3 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/710,058

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: **(2) INFORMATION FOR SEQ ID NO:X:** **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS") **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:** **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. **<210> sequence id number** **<400> sequence id number** **000**
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
11 ____	Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

Does Not Comply
Corrected Diskette Needed
see p. 6

```
 3 <110> APPLICANT: Anderson, David
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING RENILLA GFP
 7 <130> FILE REFERENCE: A-68531-1/DJB/RMS/AMS
 9 <140> CURRENT APPLICATION NUMBER: US 09/710,058
10 <141> CURRENT FILING DATE: 2000-11-10
12 <150> PRIOR APPLICATION NUMBER: US 60/164,592
13 <151> PRIOR FILING DATE: 1999-11-10
15 <160> NUMBER OF SEQ ID NOS: 85
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1079
21 <212> TYPE: DNA
22 <213> ORGANISM: Renilla muelleri
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (259)..(975)
28 <400> SEQUENCE: 1
29 ggttatacac aagtgtatcg cgtatctgca gacgcatcta gtgggattat tcgagcggta     60
31 gtatttacgt cagacctgtc taatcgaaac cacaacaaac tcttaaaata agccacattt    120
33 acataatatc taagagacgc ctcatttaag agtagtaaaa atataatata tgatagagta    180
35 tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttgttaa tgcaatcgaa    240
37 agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta      291
38                     Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
39                     1               5                  10
41 caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac      339
42 Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
43             15                  20                  25
45 cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc      387
46 His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
47         30                  35                  40
49 aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt      435
50 Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
51     45                  50                  55
53 gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc      483
54 Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe
55 60                  65                  70                  75
57 acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca      531
58 Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
59                 80                  85                  90
61 gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt      579
62 Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
63             95                  100                 105
65 gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac      627
66 Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
67         110                 115                 120
69 aga gtc gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg      675
70 Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

```
71     125                 130                 135
73 cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg      723
74 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
75 140                 145                 150                 155
77 aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac      771
78 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
79                 160                 165                 170
81 tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa      819
82 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
83             175                 180                 185
85 ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg      867
86 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
87         190                 195                 200
89 gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act      915
90 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
91     205                 210                 215
93 gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac      963
94 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
95 220                 225                 230                 235
97 gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca         1015
98 Glu Trp Val
101 aataataatt ttttaaacaa ttatcaatgt tttgtgatat gtttgtaaaa aaaaaaaaaa  1075
103 aaaa                                                             1079
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 238
108 <212> TYPE: PRT
109 <213> ORGANISM: Renilla muelleri
111 <400> SEQUENCE: 2
113 Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
114 1               5                  10                  15
117 Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
118             20                  25                  30
121 Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
122         35                  40                  45
125 Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
126     50                  55                  60
129 Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
130 65                  70                  75                  80
133 Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
134                 85                  90                  95
137 Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
138             100                 105                 110
141 Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
142         115                 120                 125
145 Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
146     130                 135                 140
149 Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
150 145                 150                 155                 160
153 Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr
```

RAW SEQUENCE LISTING DATE: 04/24/2001
PATENT APPLICATION: US/09/710,058 TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

```
154                 165                 170                 175
157 Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
158             180                 185                 190
161 Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
162         195                 200                 205
165 Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
166     210                 215                 220
169 Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
170 225                 230                 235
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 1104
175 <212> TYPE: DNA
176 <213> ORGANISM: Ptilosarcus Gurneyi
178 <400> SEQUENCE: 3
179 tcggcacgag ctggcctcca cactttagac aaaatgaacc gcaacgtatt aaagaacact     60
181 ggactgaaag agattatgtc ggcaaaagct agcgttgaag gaatcgtgaa caatcacgtt    120
183 ttttccatgg aaggatttgg aaaaggcaat gtattatttg gaaaccaatt gatgcaaatc    180
185 cgggttacaa agggaggtcc gttgccattc gctttcgata ttgtttccat agctttccaa    240
187 tacgggaatc gcactttcac gaaataccca gacgacattg cggactactt tgttcaatca    300
189 ttcccggctg gatttttcta cgaaagaaat ctacgctttg aagatggcgc cattgttgac    360
191 attcgttcag atataagttt agaagatgat aagttccact acaaagtgga gtatagaggc    420
193 aacggtttcc ctagtaacgg acccgtgatg caaaaagcca tcctcggcat ggagccatcg    480
195 tttgaggtgg tctacatgaa cagcggcgtt ctggtgggcg aagtagatct cgtttacaaa    540
197 ctcgagtcag ggaactatta ctcgtgccac atgaaaacgt tttacagatc caaaggtgga    600
199 gtgaaagaat tcccggaata tcactttatc catcatcgtc tggagaaaac ctacgtggaa    660
201 gaaggaagct tcgtggaaca acacgagacg gccattgcac aactgaccac aattggaaaa    720
203 cctctgggct cccttcatga atgggtgtag aaaatgacca atatactggg gaaaccgata    780
205 accgtttgga agcttgtgta tacaaattat ttggggtcat tttgtaatgt gtatgtgtgt    840
207 tgtatgatca atagacgtcg tcattcatag cttgaatcct tcagcaaaag aaacctcgaa    900
209 gcatattgaa acctcgaagc atattgaaac ctcgacggag agcgtaaaga gaccgcacaa    960
211 attaacgcgt ttcaaccagc agttggaatc tttaaaccga tcaaaactat taatataaat   1020
213 atatataccc tgtataactt atatatatct atatagtttg atattgatta aatctgttct   1080
215 tgatcaaaaa aaaaaaaaaa aaaa                                         1104
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 1279
220 <212> TYPE: DNA
221 <213> ORGANISM: Ptilosarcus Gurneyi
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (7)..(720)
227 <400> SEQUENCE: 4
228 gacaaa atg aac cgc aac gta tta aag aac act gga ctg aaa gag att        48
229        Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile
230        1               5                   10
232 atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt        96
233 Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe
234 15                  20                  25                  30
236 tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg       144
237 Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

```
238                35                  40                  45
240 atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac      192
241 Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp
242             50                  55                  60
244 att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac      240
245 Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr
246         65                  70                  75
248 cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt      288
249 Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe
250     80                  85                  90
252 ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att      336
253 Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile
254 95                  100                 105                 110
256 cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag      384
257 Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu
258                 115                 120                 125
260 tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc      432
261 Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala
262             130                 135                 140
264 atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc      480
265 Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly
266         145                 150                 155
268 gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac      528
269 Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn
270     160                 165                 170
272 tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg      576
273 Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val
274 175                 180                 185                 190
276 aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc      624
277 Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr
278                 195                 200                 205
280 tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca      672
281 Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala
282             210                 215                 220
284 caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg      720
285 Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
286         225                 230                 235
288 tagaaaatga ccaatatact ggggaaaatc accaatatac tggggaaaat gaccaattta    780
290 ctggggaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat    840
292 ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca    900
294 aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt    960
296 gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga   1020
298 cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc   1080
300 gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt   1140
302 aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata   1200
304 tctacatagt ttgatattga ttaaatctgt tcttgatcac taaaaaaaaa aaaaaaaaaa   1260
306 aaaaaaaaaa aaaaaaaaa                                               1279
309 <210> SEQ ID NO: 5
310 <211> LENGTH: 238
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

<212> TYPE: PRT
<213> ORGANISM: Ptilosarcus Gurneyi
<400> SEQUENCE: 5
Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
1 5 10 15
Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
20 25 30
Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
35 40 45
Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
50 55 60
Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
65 70 75 80
Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
85 90 95
Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
100 105 110
Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
115 120 125
Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
130 135 140
Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
145 150 155 160
Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
165 170 175
Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
180 185 190
Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
195 200 205
Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
210 215 220
Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
225 230 235
<210> SEQ ID NO: 6
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Aequorea victoria
<400> SEQUENCE: 6
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

<210> 8
<211> 244
<212> PRT
<213> Artificial

see item 11 on Error Summary Sheet

(sample of global error)

FYI

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

FYI

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:16

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

L:483 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1345 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:1367 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:1380 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:1405 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1425 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:1438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1444 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:1457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1463 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:1476 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:1489 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:1502 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1694 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1800 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:1921 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:1934 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:51
L:1948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1954 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:52
L:1967 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:53
L:2065 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:61
L:2078 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:62
L:2090 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:63
L:2102 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:64
L:2114 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:65
L:2128 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:66
L:2142 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:67
L:2154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:68
L:2166 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:69
L:2180 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:70
L:2194 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:71

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001
TIME: 13:20:16

Input Set : A:\A68531-1.ST25.txt
Output Set: N:\CRF3\04242001\I710058.raw

L:2208 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:72
L:2222 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:73
L:2236 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:74
L:2250 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:75
L:2264 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:76
L:2278 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:77
L:2292 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:78
L:2306 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:79
L:2320 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:80
L:2334 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:81
L:2346 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:82
L:2360 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:83
L:2374 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:84
L:2387 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:85

Application No. 09/710,058

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirement for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.82

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☒ 7. Other: See ATTACHED CRF ERROR REPORT

Applicant must provide:

☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An ~~initial~~ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☐ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

Attachment for PTO-948 (Rev. 03/01, or earlier)
6/18/01

The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

1. Correction of Informalities -- 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may NOT be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.